

341 U.S. PTO
09/776910

02/06/01

SUBSTITUTE SHEET (RULE 26)

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Lc743 I T G K V C G S E D C L Y L S V Y T N N 120
RM8con
301 -----+-----+-----+-----+-----+ 360
Lc743 ATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGAATAAT
RM8A
RM8B
RM8C
RM8con

Lc743 L N P E T K R P V L V Y I H G G G F I I 140
RM8con
361 -----+-----+-----+-----+-----+ 420
Lc743 CTAAATCCCGAAACTAAACGTCCTCGTTTGTATACATACATGGTGGTGGTTTTATTATC
RM8A
RM8B
RM8C
RM8con

Lc743 G E N H R D M Y G P D Y F I K K D V V L 160
RM8con
421 -----+-----+-----+-----+-----+ 480
Lc743 GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTTCATTAAAAAGGATGTGGTGTG
RM8A
RM8B
RM8C
RM8con

Lc743 I N I Q Y R L G A L G F L S L N S E D L 180
RM8con
481 -----+-----+-----+-----+-----+ 540
Lc743 ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTGAGAAGACCTT
RM8A
RM8B
RM8C
RM8con

Lc743 N V P G N A G L K D Q V M A L R W I K N 200
RM8con
541 -----+-----+-----+-----+-----+ 600
Lc743 AATGTGCCCCGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
RM8A
RM8B
RM8CA.....
RM8con

Figure 1 ~~continued~~

Lc743	N C A N F G G N P D N I T V F G E S A G	220
RM8con	
601	- - - - + - - - - - + - - - - - + - - - - - + - - - - - +	660
Lc743	AATTGCGCCAACCTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT	
RM8A	
RM8B	
RM8C	
RM8con	
Lc743	A A S T H Y M M L T E Q T R G L F H R G	240
RM8con	
661	- - - - + - - - - - + - - - - - + - - - - - + - - - - - +	720
Lc743	GCTGCCTCTACCCACTACATGATGTTAACCGAACAACTCGCGGTCTTTTCCATCGTGGT	
RM8A	
RM8B	
RM8C	
RM8con	
Lc743	I L M S G N A I C P W A N T Q C Q H R A	260
RM8con L	
721	- - - - + - - - - - + - - - - - + - - - - - + - - - - - +	780
Lc743	ATACTAATGTCGGGTAATGCTATTTGTCCATGGGCTAATACCCAATGTCAACATCGTGCC	
RM8A T	
RM8B T	
RM8C T	
RM8con T	
Lc743	F T L A K L A G Y K G E D N D K D V L E	280
RM8con	
781	- - - - + - - - - - + - - - - - + - - - - - + - - - - - +	840
Lc743	TTCACCTTAGCCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAA	
RM8A	
RM8B	
RM8C A	
RM8con	
Lc743	F L M K A K P Q D L I K L E E K V L T L	300
RM8con	
841	- - - - + - - - - - + - - - - - + - - - - - + - - - - - +	900
Lc743	TTTCTTATGAAAGCCAAGCCACAGGATTTAATAAACTTGAGGAAAAAGTTTTAACTCTA	
RM8A	
RM8B	
RM8C G	
RM8con	

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Lc743 E E R T N K V M F P F G P T V E P Y Q T 320
RM8con
901 -----+-----+-----+-----+-----+ 960
Lc743 GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCCTGTTGAGCCATATCAGACC
RM8A
RM8B
RM8C
RM8con

Lc743 A D C V L P K H P R E M V K T A W G N S 340
RM8con
961 -----+-----+-----+-----+-----+1020
Lc743 GCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAACTGCTTGGGGTAATTCTG
RM8A
RM8B
RM8C
RM8con

Lc743 I P T M M G N T S Y E G L F F T S I L K 360
RM8con
1021 -----+-----+-----+-----+-----+1080
Lc743 ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACCTCAATTCTTAAG
RM8A
RM8B
RM8C
RM8con

Lc743 Q M P M L V K E L E T C V N F V P S E L 380
RM8con
1081 -----+-----+-----+-----+-----+1140
Lc743 CAAATGCCTATGCTTGTTAAGGAATTGGAACTTGTGTCAATTTTGTGCCAAGTGAATTG
RM8A
RM8B
RM8C
RM8con

Lc743 A D A E R T A P E T L E M G A K I K K A 400
RM8con
1141 -----+-----+-----+-----+-----+1200
Lc743 GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT
RM8A T.....
RM8B
RM8C
RM8con

Figure 1 continued

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Lc743 H V T G E T P T A D N F M D L C S H I Y 420
RM8con
1201 -----+-----+-----+-----+-----+1260
Lc743 CATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT
RM8A
RM8B
RM8C
RM8con

Lc743 F W F P M H R L L Q L R F N H T S G T P 440
RM8con
1261 -----+-----+-----+-----+-----+1320
Lc743 TTCTGGTTCCCCATGCATCGTTTGTGCAATTACGTTTCAATCACACCTCCGGTACACCC
RM8A
RM8B
RM8C
RM8con

Lc743 V Y L Y R F D F D S E D L I N P Y R I M 460
RM8con
1321 -----+-----+-----+-----+-----+1380
Lc743 GTCTACTTGTATCGCTTCGACTTTGATTGCGGAAGATCTTATTAATCCCTATCGTATTATG
RM8A C.....C.....
RM8B C.....C.....
RM8C C.....C.....
RM8con C.....C.....

Lc743 R S G R G V K G V S H A D E L T Y F F W 480
RM8con
1381 -----+-----+-----+-----+-----+1440
Lc743 CGTAGTGGACGTGGTGTAAAGGGTGTAGTCATGCTGATGAATTAACCTATTTCTTCTGG
RM8A
RM8B
RM8C
RM8con

Lc743 N Q L A K R M P K E S R E Y K T I E R M 500
RM8con
1441 -----+-----+-----+-----+-----+1500
Lc743 AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG
RM8A
RM8B
RM8C
RM8con

E
Figure 1 continued

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Lc743 T G I W I Q F A T T G N P Y S N E I E G 520
RM8con
1501 -----+-----+-----+-----+-----+1560
Lc743 ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT
RM8A
RM8B
RM8C
RM8con

Lc743 M E N V S W D P I K K S D E V Y K C L N 540
RM8con
1561 -----+-----+-----+-----+-----+1620
Lc743 ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGACGAAGTATACAAGTGTGGAAT
RM8AT.....
RM8BT.....
RM8CT.....
RM8conT.....

Lc743 I S D E L K M I D V P E M D K I K Q W E 560
RM8con
1621 -----+-----+-----+-----+-----+1680
Lc743 ATTAGTGACGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAA
RM8AT.....G
RM8BT.....G
RM8CT.....G
RM8conT.....G

Lc743 S M F E K H R D L F * 570
RM8con
1681 -----+-----+-----+-----+1713
Lc743 TCGATGTTTGAAAAACATAGAGATTTATTTTAG
RM8ALc743/3'.....
RM8B
RM8C
RM8con

F
Figure 1 ~~continued~~

Figure 2.

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Figure 3A

Seq. ID No: 14
1 ATGACTTTTCTGAAGCAATTCATATTTTCGCCTGAAACTATGCTTTAAATGCATGGTCAAT
-----+-----+-----+-----+-----+ 60
TACTGAAAAGACTTCGTTAAGTATAAAGCGGACTTTGATACGAAATTTACGTACCAGTTA

Seq. ID No: 13
61 M T F L K Q F I F R L K L C F K C M V N -
AAATACACAAACTACCGTCTGAGTACAAATGAAACCCAAATAATCGATACTGAATATGGA
-----+-----+-----+-----+-----+ 120
TTTATGTGTTTGATGGCAGACTCATGTTTACTTTGGGTTTATTAGCTATGACTTATACCT
K Y T N Y R L S T N E T Q I I D T E Y G -
CAAATTAAGGGTGTTAAGCGAATGACCGTCTACGATGATTCTTACTACAGTTTCGAGAGT
121 -----+-----+-----+-----+-----+ 180
GTTTAATTCCCACAATTCGCTTACTGGCAGATGCTACTAAGAATGATGTCAAAGCTCTCA
Q I K G V K R M T V Y D D S Y Y S F E S -
ATACCCTATGCTAAGCCTCCAGTGGGTGAGTTGAGATTCAAGGCACCCCAGCGGCCTGTA
181 -----+-----+-----+-----+-----+ 240
TATGGGATACGATTCCGAGGTCACCCACTCAACTCTAAGTTCCGTGGGGTCGCCGGACAT
I P Y A K P P V G E L R F K A P Q R P V -
CCATGGGAGGGTGTTACGTGATTGCTGTGGGCCAGCCAACAGATCGGTACAGACAGATTTTC
241 -----+-----+-----+-----+-----+ 300
GGTACCCTCCCACATGCACTAACGACACCCGGTTCGGTTGTCTAGCCATGTCTGTCTAAAG
P W E G V R D C C G P A N R S V Q T D F -
ATAAGTGGCAAACCCACAGGTTCCGAGGATTGTCTATACCTGAATGTGTATACCAATGAC
301 -----+-----+-----+-----+-----+ 360
TATTCACCGTTTGGGTGTCCAAGCCTCCTAACAGATATGGACTTACACATATGGTTACTG
I S G K P T G S E D C L Y L N V Y T N D -
TTGAACCCAGACAAAAGGCGTCCTGTTATGGTTTTTCATCCATGGCGGAGATTTTATTTTC
361 -----+-----+-----+-----+-----+ 420
AACTTGGGTCTGTTTTCCGCAGGACAATACCAAAAAGTAGGTACCGCCTCTAAAATAAAAG
L N P D K R R P V M V F I H G G D F I F -
GGCGAAGCAAATCGTAACTGGTTTGGTCCCGACTACTTTATGAAGAAACCCGTGGTCTTG
421 -----+-----+-----+-----+-----+ 480
CCGCTTCGTTTAGCATTGACCAAACAGGGCTGATGAAATACTTCTTTGGGCACCAGAAC
G E A N R N W F G P D Y F M K K P V V L -

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GTAACCGTGCAATATCGTTTGGGTGTGTTGGGTTTCCTTAGCCTGAAATCGGAAAATCTC
481 -----+-----+-----+-----+-----+ 540
CATTGGCACGTTATAGCAAACCCACACAACCCAAAGGAATCGGACTTTAGCCTTTTAGAG
V T V Q Y R L G V L G F L S L K S E N L -
AATGTCCCCGGCAACGCTGGCCTCAAGGATCAAGTAATGGCCTTGAGATGGGTCAAGAGT
541 -----+-----+-----+-----+-----+ 600
TTACAGGGGGCGTTGCGACCGGAGTTCCTAGTTCATTACCGGAACTCTACCCAGTTCTCA
N V P G N A G L K D Q V M A L R W V K S -
AATATTGCCATTTTCGGTGGCGATGTAGACAATATTACCGTCTTCGGCGAAAAGTGCTGGT
601 -----+-----+-----+-----+-----+ 660
TTATAACGGTAAAAGCCACCGCTACATCTGTTATAATGGCAGAAGCCGCTTTCACGACCA
N I A I F G G D V D N I T V F G E S A G -
GGGGCCTCAACCCATTACATGATGATAACCGAACAGACCCGTGGTTTATTCCATCGTGGT
661 -----+-----+-----+-----+-----+ 720
CCCCGGAGTTGGGTAATGTACTACTATTGGCTTGCTCTGGGCACCAAATAAGGTAGCACCA
G A S T H Y M M I T E Q T R G L F H R G -
ATCATGATGTCCGGTAATTCCATGTGCTCATGGGCCTCTACAGAATGCCAAAGTCGTGCG
721 -----+-----+-----+-----+-----+ 780
TAGTACTACAGGCCATTAAGGTACACGAGTACCCGGAGATGTCTTACGGTTTCAGCACGC
I M M S G N S M C S W A S T E C Q S R A -
CTCACCATGGCCAAACGTGTTGGCTATAAGGGAGAGGACAATGAAAAAGATATCCTGGAA
781 -----+-----+-----+-----+-----+ 840
GAGTGGTACCGGTTTGCACAACCGATATTCCCTCTCCTGTTACTTTTTCTATAGGACCTT
L T M A K R V G Y K G E D N E K D I L E -
TTCCTAATGAAAGCCAATCCCTATGATTTGATCAAAGAGGAGCCACAAGTTTTGACACCC
841 -----+-----+-----+-----+-----+ 900
AAGGATTACTTTTCGGTTAGGGATACTAAACTAGTTTCTCCTCGGTGTTCAAACTGTGGG
F L M K A N P Y D L I K E E P Q V L T P -
GAAAGAATGCAAAAATAAGGTCATGTTTCCTTTTGGACCCACTGTAGAACCATACCAGACA
901 -----+-----+-----+-----+-----+ 960
CTTTCTTACGTTTTATTCCAGTACAAAGGAAAACCTGGGTGACATCTTGGTATGGTCTGT
E R M Q N K V M F P F G P T V E P Y Q T -
GCCGACTGTGTGGTACCCAAACCAATCAGAGAAATGGTGAAGAGCGCCTGGGGAAATTCC
961 -----+-----+-----+-----+-----+ 1020
CGGCTGACACACCATGGGTTTGGTTAGTCTCTTTACCACTTCTCGCGGACCCCTTTAAGC
A D C V V P K P I R E M V K S A W G N S -

B
Figure 3 ~~continued~~

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ATACCCACATTGATAGGCAATACCTCCTACGAAGGTTTGCTTTCCAAATCAATTGCCAAA
1021 -----+-----+-----+-----+-----+ 1080
TATGGGTGTAACCTATCCGTTATGGAGGATGCTTCCAAACGAAAGGTTTAGTTAACGGTTT

I P T L I G N T S Y E G L L S K S I A K -

CAATATCCGGAGGTTGTAAAAGAGTTGGAATCCTGTGTGAATTATGTGCCTTGGGAGTTG
1081 -----+-----+-----+-----+-----+ 1140
GTTATAGGCCTCCAACATTTTCTCAACCTTAGGACACACTTAATACACGGAACCTCAAC

Q Y P E V V K E L E S C V N Y V P W E L -

GCTGACAGTGAACGCAGTGCCCCGAAACCCTGGAGAGGGCTGCCATTGTGAAAAAGGCC
1141 -----+-----+-----+-----+-----+ 1200
CGACTGTCACCTTGCCTCACGGGGCCTTTGGGACCTCTCCCGACGGTAACACTTTTTCCGG

A D S E R S A P E T L E R A A I V K K A -

CATGTGGATGGGGAAACACCTACTCTGGATAATTTTATGGAGCTTTGCTCCTATTTCTAT
1201 -----+-----+-----+-----+-----+ 1260
GTACACCTACCCCTTTGTGGATGAGACCTATTAATAATACCTCGAAACGAGGATAAAGATA

H V D G E T P T L D N F M E L C S Y F Y -

TTCCTCTTCCCATGCATCGCTTCCTACAATTGCGCTTCAACCACACAGCTGGCACTCCC
1261 -----+-----+-----+-----+-----+ 1320
AAGGAGAAGGGGTACGTAGCGAAGGATGTTAACGCGAAGTTGGTGTGTCGACCGTGAGGG

F L F P M H R F L Q L R F N H T A G T P -

ATTTATTTGTATCGTTTCGATTTTCGATTCCGAAGAAATTATTAACCCCTATCGTATTATG
1321 -----+-----+-----+-----+-----+ 1380
TAAATAAACATAGCAAAGCTAAAGCTAAGGCTTCTTTAATAATTGGGGATAGCATAATAC

I Y L Y R F D F D S E E I I N P Y R I M -

CGTTTTGGCCGTGGCGTTAAAGGTGTAAGCCATGCCGATGAGCTAACCTATCTCTTCTGG
1381 -----+-----+-----+-----+-----+ 1440
GCAAAACCGGCACCGCAATTTCCACATTCCGCTACGGCTACTCGATTGGATAGAGAAGACC

R F G R G V K G V S H A D E L T Y L F W -

AACATTTTGTGCGAAACGCCTGCCAAAGGAAAGCCGCGAATACAAAACCATGAACGCATG
1441 -----+-----+-----+-----+-----+ 1500
TTGTAAAACAGCTTTGCGGACGGTTTCCTTTCCGGCGCTTATGTTTGGTAACTTGCGTAC

N I L S K R L P K E S R E Y K T I E R M -

GTTGGCATTGTGGACGGAATTCGCCACCACCGGCAAACCATACAGCAATGATATAGCCGGC
1501 -----+-----+-----+-----+-----+ 1560
CAACCGTAAACCTGCCTTAAGCGGTGGTGGCGCTTGGTATGTCGTTACTATATCGGCCG

V G I W T E F A T T G K P Y S N D I A G -

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Figure 3 continued

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ATGGAAAACCTCACCTGGGATCCCATAAAAAAATCCGATGATGTCTATAAATGTTTAAAT
1561 -----+-----+-----+-----+-----+ 1620
TACCTTTTGGAGTGGACCCTAGGGTATTTTTTTTAGGCTACTACAGATATTTACAAATTTA
M E N L T W D P I K K S D D V Y K C L N -
ATCGGCGATGAATTGAAAGTTATGGATTTGCCAGAAATGGATAAAATTAAACAATGGGCA
1621 -----+-----+-----+-----+-----+ 1680
TAGCCGCTACTTAACTTTCAATACCTAAACGGTCTTTACCTATTTTAATTTGTTACCCGT
I G D E L K V M D L P E M D K I K Q W A -
AGTATATTCGATAAAAAAGAAGGAATTGTTT
1681 -----+-----+-----+ 1710
TCATATAAGCTATTTTTCTTCCTTAACAAA
S I F D K K K E L F

Figure 3 continued

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Figure 4.

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Seq. ID NO: 158 MdaE7 97 QTDFFISGKPTGSEDCLYLNVTYNDLNPDKKRPVMVFIHGGGFIFGEANRN 146
|.|||.||..|||.|.||||:|.|.:|.|.:|.|.:|.|.:|.|.:|
Seq. ID NO: 43 LcaE7 97 QVDFITGKVCGSEDCLYLSVYTNLNPETKRPVLVYIHGGGFIIGENHRD 146
.
147 WYGPDPYFMKKPVVLVTVQYRLGVLGFLSLKSENLNVPGNAGLKDQVMALR 196
|||.|.:|.|.:|.|.:|.|.:|.|.:|.|.:|.|.:|.|.:|
147 MYGPDPYFIKDVVLINIYRLGALGFLSLNSEDLNVPGNAGLKDQVMALR 196
.
197 WFKSNI AIFGGDV DNITVFGESAGGASTHYMMITEQTRGLFHRGIMMSGN 246
|.:|.|. |||.:|.|.:|.|.:|.|.:|.|.:|.|.:|.|.:|
197 WIKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRGILMSGN 246
↓
247 SMCSSASTECQSRAL TMAKRVGYKGEENEKDILEFLMKANPYDLIKEEPQ 296
.:|. |.:| |||.:|.|.:|.|.:|.|.:|.|.:|.|.:|.|.:|
247 AICPLANTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPDLIKLEEK 296

297 VLTPERM 303
||| |.
297 VLTLEER 303

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